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FIGURE 1

A

AHASL1D

WT

CACGTGCTGCCTATGATCCCAAGCGGTGGTGCTTTCAAGGAC
H V L P M I P S G G A F K D

MUT

CACGTGCTGCCTATGATCCCAAACGGTGGTGCTTTCAAGGAC
H V L P M I P N G G A F K D

B

AHASL1B

WT

CACGTGCTGCCTATGATCCCAAGCGGTGGTGCTTTTAAGGAC
H V L P M I P S G G A F K D

MUT

CACGTGCTGCCTATGATCCCAAACGGTGGTGCTTTTAAGGAC
H V L P M I P N G G A F K D

C

AHASL1A

WT

CACGTGCTGCCTATGATCCCAAGCGGTGGTGCTTTCAAGGAC
H V L P M I P S G G A F K D

MUT

CACGTGCTGCCTATGATCCCAAACGGTGGTGCTTTCAAGGAC
H V L P M I P N G G A F K D

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FIGURE 2

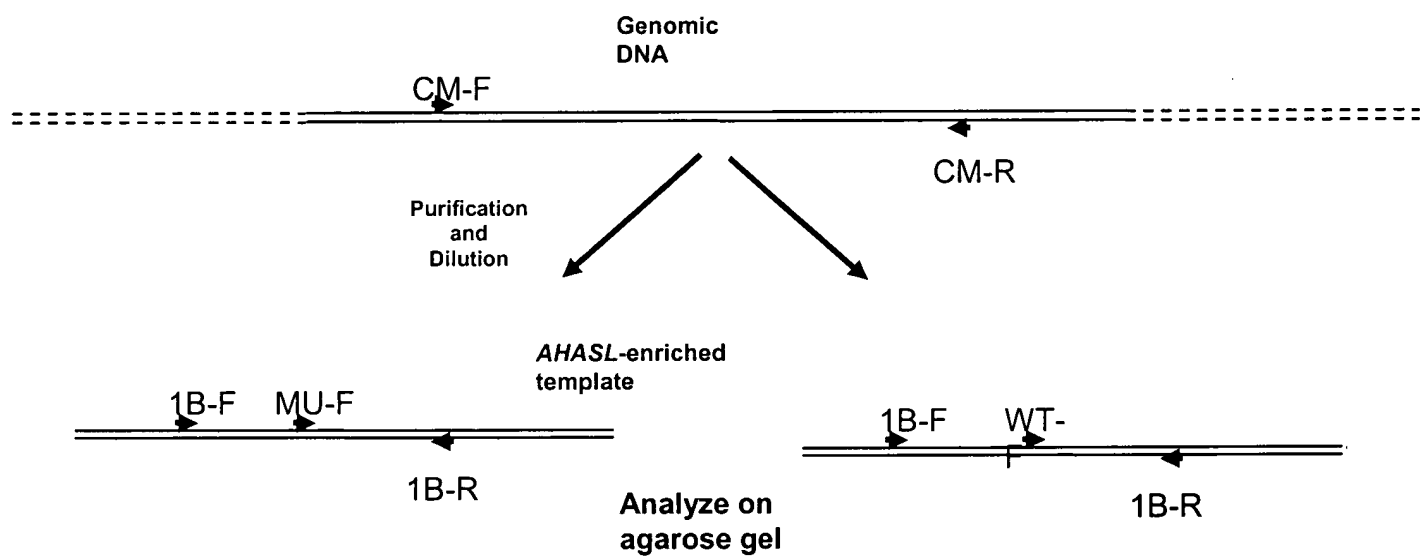


FIGURE 3 (sheet 1 of 3)

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» AHASL1B (1251) TTTGGTCCATGGCACAAGGAGTTGGATCAGCAGAAGAGGGAGTTTCCTCT
» AHASL1D (945) TTTGGTCCATGGCACAAGGAGTTGGATCAGCAGAAGAGGGAGTTTCCTCT
» AHASL1A (1058) TTTGGTCCATGGCACAAGGAGTTGGATCAGCAGAAGAGGGAGTTTCCTCT
(1251)

» CM-F (1) CCGCCGCAATATGCTATCCA>>
» AHASL1B (1301) AGGATTCAAGACTTTTGGTGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1D (995) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1A (1108) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
(1301) +

» AHASL1B (1351) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACCGGTGTTGGG
» AHASL1D (1045) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACTGGTGTGGG
» AHASL1A (1158) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCTACTGGTGTGGG
(1351) + +

» AHASL1B (1401) CAGCATCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1D (1095) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1A (1208) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
(1401) +

» AHASL1B (1451) GTGGCTGTCTTCATCCGGTTTGGGTGCAATGGGATTTGGGTTGCCAGCTG
» AHASL1D (1145) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTTGGGTTACCAGCTG
» AHASL1A (1258) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTTGGGTTACCAGCTG
(1451) + + + +

» AHASL1B (1501) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1D (1195) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1A (1308) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
(1501)

» AHASL1B (1551) GGGGATGGTAGTTTCCTCATGAACATTTCAGGAGTTGGCGTTGATCCGTAT
» AHASL1D (1245) GGTGATGGTAGTTTCCTCATGAACATTTCAGGAGTTGGCGTTGATCCGCAT
» AHASL1A (1358) GGAGATGGTAGTTTCCTCATGAACATTTCAGGAGTTGGCATTGATCCGTAT
(1551) + + +

» AHASL1B (1601) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
» AHASL1D (1295) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
» AHASL1A (1408) TGAGAACCTCCCTGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
(1601) +

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FIGURE 3 (sheet 2 of 3)

» AHASL1B	(1651)	TGGTGGTGCAAGTGGGAGGATAGGTTTTACAAGGCCAACCGGGCGCACACA
» AHASL1D	(1345)	TGGTGGTGCAAGTGGGAGGATAGGTTTTACAAGGCCAACCGGGCGCACACA
» AHASL1A	(1458)	TGGTGGTGCAATGGGAGGATAGGTTTTACAAGGCCAACCGGGCGCACACA
	(1651)	+ +
» AHASL1B	(1701)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC
» AHASL1D	(1395)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC
» AHASL1A	(1508)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC
	(1701)	
» AHASL1B	(1751)	GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG
» AHASL1D	(1445)	GATTGCTAAAGGATTCAACGTTCCAGCAGTTCGAGTGACGAAGAAGAGCG
» AHASL1A	(1558)	GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG
	(1751)	+ +
» AHASL1B	(1801)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG
» AHASL1D	(1495)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG
» AHASL1A	(1608)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG
	(1801)	
» AHASL1B	(1851)	TTGGATATCATTGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG
» AHASL1D	(1545)	TTGGATATCATAGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG
» AHASL1A	(1658)	TTGGATATCATCGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG
	(1851)	+
» AHASL1B	(1901)	CGGTGGTGCTTTTAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT
» AHASL1D	(1595)	CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT
» AHASL1A	(1708)	CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT
	(1901)	+
» AHASL1B	(1951)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
» AHASL1D	(1645)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
» AHASL1A	(1758)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
	(1951)	
» AHASL1B	(2001)	TGATACCTGCGTGTTGTATCAACTACTGGGGGTTCAACTGTGAACCATGC
» AHASL1D	(1695)	TGATGCCCCGCGTGTTGTATCAACTACTAGGGGTTCAACTGTGARCCATGC
» AHASL1A	(1808)	TGGTGCCCCGCGTGTTGTATCAACTACTAGGGGTTCAACTGTGAACCATGC
	(2001)	+ + + + +
» AHASL1B	(2051)	GTTTTCTAGTTTGCTTGTTTCATTCATATAAGCTTGTGTTACTTAGTTCC
» AHASL1D	(1745)	GTTTTCTAGTTTGCTTGTTTCATTCATATAAGCTTGTGTTACTTAGTTCC
» AHASL1A	(1858)	GTTTTCTAGTTTGCTTGTTTCATTCATATAAGCTTGTGTTACTTAGTTCC
	(2051)	+

FIGURE 3 (sheet 3 of 3)

» AHASL1B	(2101)	GAACCGTGTAGTTTTGTAGTCTCTGTTCTCTTTTGTAGGGAYGTGCTGTC	
» AHASL1D	(1795)	GAACCCTGTAGTTTTGTAGTCTATGTTCTCTTTTGTAGGGATGTGCTGTC	
» AHASL1A	(1908)	GAACCCTGTAGCTTTGTAGTCTATGCTATCTTTTGTAGGGATGTGCTGTC	
	(2101)	+ + + + +	+
» AHASL1B	(2151)	ATAARATATCATGCAAGTTTCTTGTCTACATATCAATAATAAGCACTTC	
» AHASL1D	(1845)	ATAARATRTCATGCAAGTTTCTTGTCTACATATCAATAATAAGTACTTC	
» AHASL1A	(1958)	ATAAAATATCATGCAAGTTTCTTGTCTACATATCAATAATAAGTACTTC	
« CM-R	(1)	<u><<CATGCAAGTTTCTTGTCTA</u>	
	(2151)	+ +	+
» AHASL1B	(2201)	CATGGAGCAAAAAAAAAAAAAAAAAAAAAAAAAA	
» AHASL1D	(1895)	CATGCAGTAAAAAAAAAAAAAAAAAAAAAAAAA	
» AHASL1A	(2008)	CATGGAAAAAAAAAAAAAAAAAAAAAAAAA	
	(2201)	+ ++	

FIGURE 4 (sheet 1 of 3)

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» AHASL1B (1301) AGGATTCAAGACTTTTGGTGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1D (995) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1A (1108) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
      (1301)                                     +

      » 1AD-F (1)                                     GGGAGGCGATCATTGCCAC>>
» AHASL1B (1351) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACCGGTGTTGGG
» AHASL1D (1045) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACTGGTGTGGG
» AHASL1A (1158) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCTACTGGTGTGGG
      (1351)                                     + +

      » 1B-F (1)                                     GCGA
» AHASL1B (1401) CAGCATCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1D (1095) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1A (1208) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
      (1401)                                     +

      » 1B-F (6) GTGGCTGTCTTCATC>>
» AHASL1B (1451) GTGGCTGTCTTCATCCGGTTTGGGTGCAATGGGATTTGGGTTGCCAGCTG
» AHASL1D (1145) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTTGGGTTACCAGCTG
» AHASL1A (1258) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTTGGGTTACCAGCTG
      (1451)                                     + + + +

» AHASL1B (1501) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1D (1195) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1A (1308) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
      (1501)

» AHASL1B (1551) GGGGATGGTAGTTTCCTCATGAACATTTCAGGAGTTGGCGTTGATCCGTAT
» AHASL1D (1245) GGTGATGGTAGTTTCCTCATGAACATTTCAGGAGTTGGCGTTGATCCGCAT
» AHASL1A (1358) GGAGATGGTAGTTTCCTCATGAACATTTCAGGAGTTGGCATTGATCCGTAT
      (1551) + + +

» AHASL1B (1601) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
» AHASL1D (1295) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
» AHASL1A (1408) TGAGAACCTCCCTGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
      (1601) +

      « 1A-R (1)
» AHASL1B (1651) TGGTGGTGCAGTGGGAGGATAGGTTTTACAAGGCCAACCGGGCGCACACA
» AHASL1D (1345) TGGTGGTGCAGTGGGAGGATAGGTTTTACAAGGCCAATCGGGCGCACACA
» AHASL1A (1458) TGGTGGTGCATGGGAGGATAGGTTTTACAAGGCCAATCGGGCGCACACA
      (1651) + +

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FIGURE 4 (sheet 2 of 3)

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» AHASL1B (1701) TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC
» AHASL1D (1395) TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC
» AHASL1A (1508) TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC
(1701)

» AHASL1B (1751) GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG
» AHASL1D (1445) GATTGCTAAAGGATTCAACGTTCCAGCAGTTCGAGTGACGAAGAAGAGCG
» AHASL1A (1558) GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG
(1751) + +

» AHASL1B (1801) AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG
» AHASL1D (1495) AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG
» AHASL1A (1608) AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG
(1801)

» WT-F (1) GTGCTGCCTATGATCCGAAG
» MU-F (1) CGTGCTGCCTATGATCCGAAC
» AHASL1B (1851) TTGGATATCATTGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG
» AHASL1D (1545) TTGGATATCATAGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG
» AHASL1A (1658) TTGGATATCATCGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG
(1851) + + +

» AHASL1B (1901) CGGTGGTGCTTTTAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT
» AHASL1D (1595) CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT
» AHASL1A (1708) CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT
(1901) +

» AHASL1B (1951) ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
» AHASL1D (1645) ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
» AHASL1A (1758) ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
Contig 1 (1951) ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
(1951)

» AHASL1B (2001) TGATACCTGCGTGTTGTATCAACTACTGGGGGTTCAACTGTGAACCATGC
» AHASL1D (1695) TGATGCCCCGCGTGTTGTATCAACTACTAGGGGTTCAACTGTGARCCATGC
» AHASL1A (1808) TGGTGCCCCGCGTGTTGTATCAACTACTAGGGGTTCAACTGTGAACCATGC
« 1B-R (1) <<ACCTGCGTGTTGTATCAACTACT
(2001) + + + + +

» AHASL1B (2051) GTTTTCTAGTTTGCTTGTTTCATTTCATATAAGCTTGTGTTACTTAGTTCC
» AHASL1D (1745) GTTTTCTAGTTTGCTTGTTTCATTTCATATAAGCTTGTGTTACTTAGTTCC
» AHASL1A (1858) GTTTTCTAGTTTGCTTGTTTCATTTCATATAAGCTTGTGTTACTTAGTTCC
(2051) +

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FIGURE 4 (sheet 3 of 3)

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» AHASL1B (2101) GAACCGTAGTTTTGTAGTCTCTGTTCTCTTTTGTAGGGAYGTGCTGTC
» AHASL1D (1795) GAACCCTGTAGTTTTGTAGTCTATGTTCTCTTTTGTAGGGATGTGCTGTC
» AHASL1A (1908) GAACCCTGTAGCTTTGTAGTCTATGCTATCTTTTGTAGGGATGTGCTGTC
    « 1D-R (1)                                     <<ATCTTCTCTTTTGTAGGGATGTC
    « 1A-R (1)                                     <<CTATCTTTTGTAGGGATGTCGTG
    (2101)          +      +                      + ++ +                      +

» AHASL1B (2151) ATAARATATCATGCAAGTTTCTTGTCTACATATCAATAATAAGCACTTC
» AHASL1D (1845) ATAARATRTCATGCAAGTTTCTTGTCTACATATCAATAATAAGTACTTC
» AHASL1A (1958) ATAAATATCATGCAAGTTTCTTGTCTACATATCAATAATAAGTACTTC
    (2151)          +      +                      +

» AHASL1B (2201) CATGGAGCAAAAAAAAAAAAAAAAAAAAAAAAAA
» AHASL1D (1895) CATGCAGTAAAAAAAAAAAAAAAAAAAAAAAAA
» AHASL1A (2008) CATGGAAAAAAAAAAAAAAAAAAAAAAAAA
Contig 1 (2201) CATGSARHAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 5

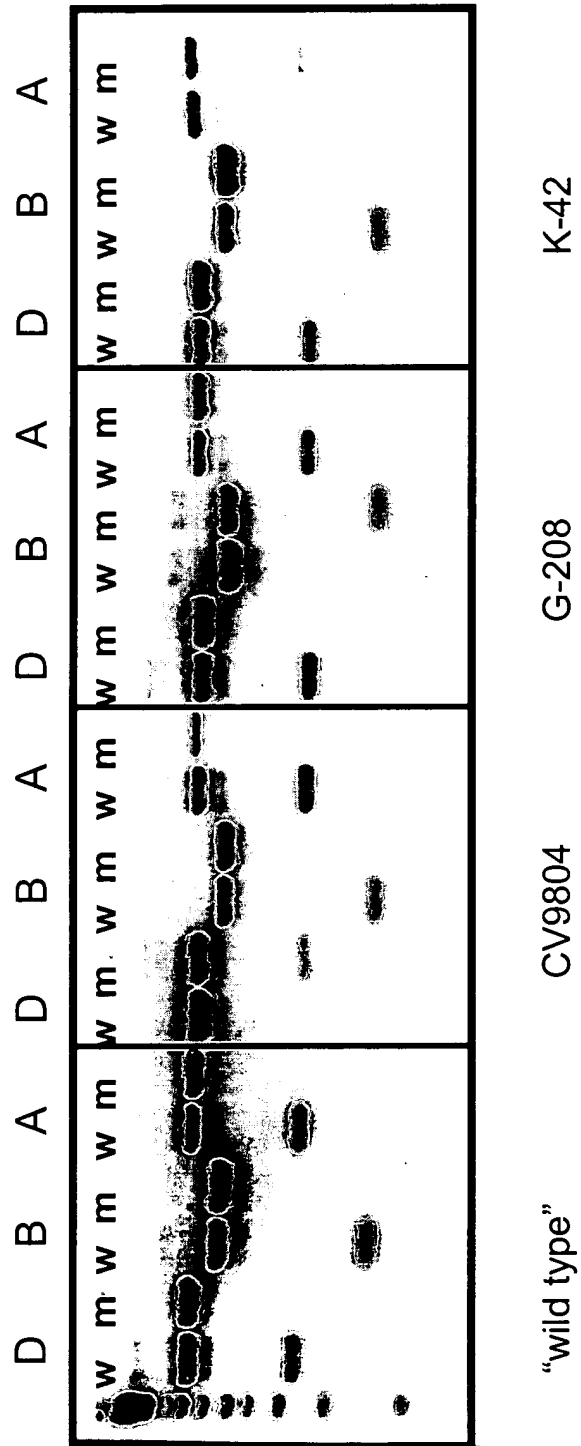


FIGURE 6

	Hexaploid L1D	Hexaploid L1B	Hexaploid L1A	Tetraploid L1B	Tetraploid L1A
Hexaploid L1D	100%	97.8%	98.2%	97.4%	97.8%
Hexaploid L1B		100%	97.7%	99.4%	97.3%
Hexaploid L1A			100%	97.3%	99.6%
Tetraploid L1B				100%	97.6%
Tetraploid L1A					100%